

## SEQUENCE LISTING

### (1) GENERAL INFORMATION:

(i) APPLICANT: Tormo, Mar  
Tari, Ana M.  
Lopez-Berestein, Gabriel

(ii) TITLE OF INVENTION: INHIBITION OF Bcl-2 PROTEIN EXPRESSION BY  
LIPOSOMAL ANTISENSE OLIGODEOXYNUCLEOTIDES

(iii) NUMBER OF SEQUENCES: 7

(iv) CORRESPONDENCE ADDRESS:  
(A) ADDRESSEE: Arnold, White & Durkee  
(B) STREET: P.O. Box 4433  
(C) CITY: Houston  
(D) STATE: Texas  
(E) COUNTRY: United States of America  
(F) ZIP: 77210

(v) COMPUTER READABLE FORM:  
(A) MEDIUM TYPE: Floppy disk  
(B) COMPUTER: IBM PC compatible  
(C) OPERATING SYSTEM: PC-DOS/MS-DOS  
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:  
(A) APPLICATION NUMBER: US Unknown  
(B) FILING DATE: Concurrently Herewith  
(C) CLASSIFICATION: Unknown

(viii) ATTORNEY/AGENT INFORMATION:  
(A) NAME: Wilson, Mark B.  
(B) REGISTRATION NUMBER: 37,259  
(C) REFERENCE/DOCKET NUMBER: UTXC:504

(ix) TELECOMMUNICATION INFORMATION:  
(A) TELEPHONE: (512) 418-3000  
(B) TELEFAX: (512) 474-7577

### (2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 18 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CAGCGTGCGC CATCCTTC

18

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

ACGGTCCGCC ACTCCTTCCC

20

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CTGAAGGGCT TCTTCC

16

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5086 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1459..2175

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

GCGCCCGCCC CTCCGCGCCG CCTGCCCCGCC CGCCCGCCGC GCTCCCGCCC GCCGCTCTCC	60
GTGGCCCCGC CGCGCTGCCG CCGCCGCCGC TGCCAGCGAA GGTGCCGGGG CTCCGGGCCC	120
TCCCTGCCGG CGGCCGTGAG CGCTCGGAGC GAACTGCGCG ACGGGAGGTC CGGGAGGCGA	180
CCGTAGTCGC GCCGCCGCGC AGGACCAGGA GGAGGAGAAA GGGTGCGCAG CCCGGAGGCG	240
GGGTGCGCCG GTGGGGTGCA GCGGAAGAGG GGGTCCAGGG GGGAGAACTT CGTAGCAGTC	300
ATCCTTTTTA GGAAAAGAGG GAAAAAATAA AACCTCCCC CACCACCTCC TTCTCCCCAC	360

	CCCTCGCCGC ACCACACACA GCGCGGGCTT CTAGCGCTCG GCACCGGCGG GCCAGGCGCG	420
	TCCTGCCTTC ATTTATCCAG CAGCTTTTCG GAAAATGCAT TTGCTGTTTCG GAGTTTAATC	480
5	AGAAGACGAT TCCTGCCTCC GTCCCCGGCT CCTTCATCGT CCCATCTCCC CTGTCTCTCT	540
	CCTGGGGAGG CGTGAAGCGG TCCCGTGGAT AGAGATTCAT GCCTGTGTCC GCGCGTGTGT	600
10	GCGCGCGTAT AAATTGCCGA GAAGGGGAAA ACATCACAGG ACTTCTGCGA ATACCGGACT	660
	GAAAATTGTA ATTCATCTGC CGCCGCCGCT GCCAAAAAAA AACTCGAGCT CTTGAGATCT	720
	CCGGTTGGGA TTCCTGCGGA TTGACATTTT TGTGAAGCAG AAGTCTGGGA ATCGATCTGG	780
15	AAATCCTCCT AATTTTTACT CCCTCTCCCC CCGACTCCTG ATTCATTGGG AAGTTTCAAA	840
	TCAGCTATAA CTGGAGAGTG CTGAAGATTG ATGGGATCGT TGCCTTATGC ATTTGTTTTG	900
20	GTTTTACAAA AAGGAAACTT GACAGAGGAT CATGCTGTAC TTAAAAAATA CAAGTAAGTC	960
	TCGCACAGGA AATTGGTTTA ATGTAACTTT CAATGGAAAC CTTTGAGATT TTTTACTTAA	1020
	AGTGCATTCG AGTAAATTTA ATTTCCAGGC AGCTTAATAC ATTGTTTTTA GCCGTGTTAC	1080
25	TTGTAGTGTG TATGCCCTGC TTTCACTCAG TGTGTACAGG GAAACGCACC TGATTTTTTA	1140
	CTTATTAGTT TGTTTTTTCT TTAACCTTTC AGCATCACAG AGGAAGTAGA CTGATATTAA	1200
30	CAATACTTAC TAATAATAAC GTGCCTCATG AAATAAAGAT CCGAAAGGAA TTGGAATAAA	1260
	AATTCCTGC GTCTCATGCC AAGAGGGAAA CACCAGAATC AAGTGTTCCG CGTGATTGAA	1320
	GACACCCCTT CGTCCAAGAA TGCAAAGCAC ATCCAATAAA ATAGCTGGAT TATAACTCCT	1380
35	CTTCTTTCTC TGGGGGCCGT GGGGTGGGAG CTGGGGCGAG AGGTGCCGTT GGCCCCCGTT	1440
	GCTTTTCCTC TGGGAAGG ATG GCG CAC GCT GGG AGA ACG GGG TAC GAC AAC	1491
	Met Ala His Ala Gly Arg Thr Gly Tyr Asp Asn	
	1 5 10	
40	CGG GAG ATA GTG ATG AAG TAC ATC CAT TAT AAG CTG TCG CAG AGG GGC	1539
	Arg Glu Ile Val Met Lys Tyr Ile His Tyr Lys Leu Ser Gln Arg Gly	
	15 20 25	
45	TAC GAG TGG GAT GCG GGA GAT GTG GGC GCC GCG CCC CCG GGG GCC GCC	1587
	Tyr Glu Trp Asp Ala Gly Asp Val Gly Ala Ala Pro Pro Gly Ala Ala	
	30 35 40	
50	CCC GCA CCG GGC ATC TTC TCC TCC CAG CCC GGG CAC ACG CCC CAT CCA	1635
	Pro Ala Pro Gly Ile Phe Ser Ser Gln Pro Gly His Thr Pro His Pro	
	45 50 55	

	GCC GCA TCC CGC GAC CCG GTC GCC AGG ACC TCG CCG CTG CAG ACC CCG	1683
	Ala Ala Ser Arg Asp Pro Val Ala Arg Thr Ser Pro Leu Gln Thr Pro	
	60 65 70 75	
5	GCT GCC CCC GGC GCC GCC GCG GGG CCT GCG CTC AGC CCG GTG CCA CCT	1731
	Ala Ala Pro Gly Ala Ala Ala Gly Pro Ala Leu Ser Pro Val Pro Pro	
	80 85 90	
10	GTG GTC CAC CTG GCC CTC CGC CAA GCC GGC GAC GAC TTC TCC CGC CGC	1779
	Val Val His Leu Ala Leu Arg Gln Ala Gly Asp Asp Phe Ser Arg Arg	
	95 100 105	
15	TAC CGC GGC GAC TTC GCC GAG ATG TCC AGC CAG CTG CAC CTG ACG CCC	1827
	Tyr Arg Gly Asp Phe Ala Glu Met Ser Ser Gln Leu His Leu Thr Pro	
	110 115 120	
	TTC ACC GCG CGG GGA CGC TTT GCC ACG GTG GTG GAG GAG CTC TTC AGG	1875
	Phe Thr Ala Arg Gly Arg Phe Ala Thr Val Val Glu Glu Leu Phe Arg	
	125 130 135	
20	GAC GGG GTG AAC TGG GGG AGG ATT GTG GCC TTC TTT GAG TTC GGT GGG	1923
	Asp Gly Val Asn Trp Gly Arg Ile Val Ala Phe Phe Glu Phe Gly Gly	
	140 145 150 155	
25	GTC ATG TGT GTG GAG AGC GTC AAC CGG GAG ATG TCG CCC CTG GTG GAC	1971
	Val Met Cys Val Glu Ser Val Asn Arg Glu Met Ser Pro Leu Val Asp	
	160 165 170	
30	AAC ATC GCC CTG TGG ATG ACT GAG TAC CTG AAC CGG CAC CTG CAC ACC	2019
	Asn Ile Ala Leu Trp Met Thr Glu Tyr Leu Asn Arg His Leu His Thr	
	175 180 185	
35	TGG ATC CAG GAT AAC GGA GGC TGG GAT GCC TTT GTG GAA CTG TAC GGC	2067
	Trp Ile Gln Asp Asn Gly Gly Trp Asp Ala Phe Val Glu Leu Tyr Gly	
	190 195 200	
40	CCC AGC ATG CGG CCT CTG TTT GAT TTC TCC TGG CTG TCT CTG AAG ACT	2115
	Pro Ser Met Arg Pro Leu Phe Asp Phe Ser Trp Leu Ser Leu Lys Thr	
	205 210 215	
	CTG CTC AGT TTG GCC CTG GTG GGA GCT TGC ATC ACC CTG GGT GCC TAT	2163
	Leu Leu Ser Leu Ala Leu Val Gly Ala Cys Ile Thr Leu Gly Ala Tyr	
	220 225 230 235	
45	CTG AGC CAC AAG TGAAGTCAAC ATGCCTGCCC CAAACAAATA TGCAAAAGGT	2215
	Leu Ser His Lys	
50	TCACTAAAGC AGTAGAAATA ATATGCATTG TCAGTGATGT ACCATGAAAC AAAGCTGCAG	2275
	GCTGTTTAAG AAAAAATAAC ACACATATAA ACATCACACA CACAGACAGA CACACACACA	2335
	CACAACAATT AACAGTCTTC AGGCAAAACG TCGAATCAGC TATTTACTGC CAAAGGGAAA	2395

	TATCATTAT	TTTTTACATT	ATTAAGAAAA	AAGATTTATT	TATTTAAGAC	AGTCCCATCA	2455
	AAACTCCGTC	TTTGGAATC	CGACCACTAA	TTGCCAAACA	CCGCTTCGTG	TGGCTCCACC	2515
5	TGGATGTTCT	GTGCCTGTAA	ACATAGATTC	GCTTTCCATG	TTGTTGGCCG	GATCACCATC	2575
	TGAAGAGCAG	ACGGATGGAA	AAAGGACCTG	ATCATTGGGG	AAGCTGGCTT	TCTGGCTGCT	2635
10	GGAGGCTGGG	GAGAAGGTGT	TCATTCACCTT	GCATTTCTTT	GCCCTGGGGG	CGTGATATTA	2695
	ACAGAGGGAG	GGTTCCTG	GGGGGAAGTC	CATGCCTCCC	TGGCCTGAAG	AAGAGACTCT	2755
	TTGCATATGA	CTCACATGAT	GCATACCTGG	TGGGAGGAAA	AGAGTTGGGA	ACTTCAGATG	2815
15	GACCTAGTAC	CCACTGAGAT	TTCCACGCCG	AAGGACAGCG	ATGGGAAAAA	TGCCCTTAAA	2875
	TCATAGGAAA	GTATTTTTTT	AAGCTACCAA	TTGTGCCGAG	AAAAGCATTT	TAGCAATTTA	2935
20	TACAATATCA	TCCAGTACCT	TAAACCCTGA	TTGTGTATAT	TCATATATTT	TGGATACGCA	2995
	CCCCCAACT	CCAATACTG	GCTCTGTCTG	AGTAAGAAAC	AGAATCCTCT	GGAACCTGAG	3055
	GAAGTGAACA	TTTCGGTGAC	TTCCGATCAG	GAAGGCTAGA	GTTACCCAGA	GCATCAGGCC	3115
25	GCCACAAGTG	CCTGCTTTTA	GGAGACCGAA	GTCCGCAGAA	CCTACCTGTG	TCCCAGCTTG	3175
	GAGGCCTGGT	CCTGGAACTG	AGCCGGGCCC	TACTGGCCT	CCTCCAGGGA	TGATCAACAG	3235
30	GGTAGTGTGG	TCTCCGAATG	TCTGGAAGCT	GATGGATGGA	GCTCAGAATT	CCACTGTCAA	3295
	GAAAGAGCAG	TAGAGGGGTG	TGGCTGGGCC	TGTCACCCTG	GGGCCCTCCA	GGTAGGCCCC	3355
	TTTTCACGTG	GAGCATAGGA	GCCACGACCC	TTCTTAAGAC	ATGTATCACT	GTAGAGGGAA	3415
35	GGAACAGAGG	CCCTGGGCCT	TCCTATCAGA	AGGACATGGT	GAAGGCTGGG	AACGTGAGGA	3475
	GAGGCAATGG	CCACGGCCCA	TTTTGGCTGT	AGCACATGGC	ACGTTGGCTG	TGTGGCCTTG	3535
40	GCCACCTGTG	AGTTTAAAGC	AAGGCTTTAA	ATGACTTTGG	AGAGGGTCAC	AAATCCTAAA	3595
	AGAAGCATTG	AAGTGAGGTG	TCATGGATTA	ATTGACCCCT	GTCTATGGAA	TTACATGTAA	3655
	AACATTATCT	TGTCACTGTA	GTTTGGTTTT	ATTTGAAAAC	CTGACAAAAA	AAAAGTTCCA	3715
45	GGTGTGGAAT	ATGGGGGTTA	TCTGTACATC	CTGGGGCATT	AAAAAAAAT	CAATGGTGGG	3775
	GAACTATAAA	GAAGTAACAA	AAGAAGTGAC	ATCTTCAGCA	AATAAACTAG	GAAATTTTTT	3835
50	TTTCTTCCAG	TTTAGAATCA	GCCTTGAAAC	ATTGATGGAA	TAACCTGTG	GCATTATTGC	3895
	ATTATATACC	ATTTATCTGT	ATTAACCTTG	GAATGTACTC	TGTTCAATGT	TTAATGCTGT	3955
	GGTTGATATT	TCGAAAGCTG	CTTTAAAAAA	ATACATGCAT	CTCAGCGTTT	TTTTGTTTTT	4015

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AATTGTATTT AGTTATGGCC TATACACTAT TTGTGAGCAA AGGTGATCGT TTTCTGTTTG 4075  
AGATTTTAT CTCTTGATTC TTCAAAAGCA TTCTGAGAAG GTGAGATAAG CCCTGAGTCT 4135  
5 CAGCTACCTA AGAAAAACCT GGATGTCACT GGCCACTGAG GAGCTTTGTT TCAACCAAGT 4195  
CATGTGCATT TCCACGTCAA CAGAATTGTT TATTGTGACA GTTATATCTG TTGTCCCTTT 4255  
10 GACCTTGTTT CTTGAAGGTT TCCTCGTCCC TGGGCAATTC CGCATTTAAT TCATGGTATT 4315  
CAGGATTACA TGCATGTTTG GTTAAACCCA TGAGATTCAT TCAGTTAAAA ATCCAGATGG 4375  
CGAATGACCA GCAGATTCAA ATCTATGGTG GTTTGACCTT TAGAGAGTTG CTTTACGTGG 4435  
15 CCTGTTTCAA CACAGACCCA CCCAGAGCCC TCCTGCCCTC CTTCCGCGGG GGCTTTCTCA 4495  
TGGCTGTCCT TCAGGGTCTT CCTGAAATGC AGTGGTCGTT ACGCTCCACC AAGAAAGCAG 4555  
GAAACCTGTG GTATGAAGCC AGACCTCCCC GCGGGGCTC AGGGAACAGA ATGATCAGAC 4615  
20 CTTTGAATGA TTCTAATTTT TAAGCAAAAT ATTATTTTAT GAAAGGTTTA CATTGTCAAA 4675  
GTGATGAATA TGGAATATCC AATCCTGTGC TGCTATCCTG CCAAATCAT TTTAATGGAG 4735  
25 TCAGTTTGCA GTATGCTCCA CGTGGTAAGA TCCTCCAAGC TGCTTTAGAA GTAACAATGA 4795  
AGAACGTGGA CGTTTTTAAT ATAAAGCCTG TTTTGTCTTT TGTTGTTGTT CAAACGGGAT 4855  
TCACAGAGTA TTTGAAAAAT GTATATATAT TAAGAGGTCA CGGGGGCTAA TTGCTAGCTG 4915  
30 GCTGCCTTTT GCTGTGGGGT TTTGTTACCT GGTTTTAATA ACAGTAAATG TGCCAGCCT 4975  
CTTGCCCCA GAACTGTACA GTATTGTGGC TGCACTTGCT CTAAGAGTAG TTGATGTTGC 5035  
35 ATTTTCCTTA TTGTTAAAAA CATGTTAGAA GCAATGAATG TATATAAAG C 5086

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 239 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Met Ala His Ala Gly Arg Thr Gly Tyr Asp Asn Arg Glu Ile Val Met  
1 5 10 15  
Lys Tyr Ile His Tyr Lys Leu Ser Gln Arg Gly Tyr Glu Trp Asp Ala  
20 25 30

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Gly Asp Val Gly Ala Ala Pro Pro Gly Ala Ala Pro Ala Pro Gly Ile  
35 40 45

5 Phe Ser Ser Gln Pro Gly His Thr Pro His Pro Ala Ala Ser Arg Asp  
50 55 60

Pro Val Ala Arg Thr Ser Pro Leu Gln Thr Pro Ala Ala Pro Gly Ala  
65 70 75 80

10 Ala Ala Gly Pro Ala Leu Ser Pro Val Pro Pro Val Val His Leu Ala  
85 90 95

Leu Arg Gln Ala Gly Asp Asp Phe Ser Arg Arg Tyr Arg Gly Asp Phe  
100 105 110

15 Ala Glu Met Ser Ser Gln Leu His Leu Thr Pro Phe Thr Ala Arg Gly  
115 120 125

20 Arg Phe Ala Thr Val Val Glu Glu Leu Phe Arg Asp Gly Val Asn Trp  
130 135 140

Gly Arg Ile Val Ala Phe Phe Glu Phe Gly Gly Val Met Cys Val Glu  
145 150 155 160

25 Ser Val Asn Arg Glu Met Ser Pro Leu Val Asp Asn Ile Ala Leu Trp  
165 170 175

Met Thr Glu Tyr Leu Asn Arg His Leu His Thr Trp Ile Gln Asp Asn  
180 185 190

30 Gly Gly Trp Asp Ala Phe Val Glu Leu Tyr Gly Pro Ser Met Arg Pro  
195 200 205

Leu Phe Asp Phe Ser Trp Leu Ser Leu Lys Thr Leu Leu Ser Leu Ala  
210 215 220

Leu Val Gly Ala Cys Ile Thr Leu Gly Ala Tyr Leu Ser His Lys  
225 230 235

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 911 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 147..761

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

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	TGATTGAAGA CACCCCCTCG TCCAAGAATG CAAAGCACAT CCAATAAAAT AGCTGGATTA	60
	TAACCTCTCT TCTTTCTCTG GGGGCCGTGG GGTGGGAGCT GGGGCGAGAG GTGCCGTTGG	120
5	CCCCCGTTGC TTTTCCTCTG GGAAGG ATG GCG CAC GCT GGG AGA ACG GGG TAC Met Ala His Ala Gly Arg Thr Gly Tyr 1 5	173
10	GAC AAC CGG GAG ATA GTG ATG AAG TAC ATC CAT TAT AAG CTG TCG CAG Asp Asn Arg Glu Ile Val Met Lys Tyr Ile His Tyr Lys Leu Ser Gln 10 15 20 25	221
15	AGG GGC TAC GAG TGG GAT GCG GGA GAT GTG GGC GCC GCG CCC CCG GGG Arg Gly Tyr Glu Trp Asp Ala Gly Asp Val Gly Ala Ala Pro Pro Gly 30 35 40	269
20	GCC GCC CCC GCA CCG GGC ATC TTC TCC TCC CAG CCC GGG CAC ACG CCC Ala Ala Pro Ala Pro Gly Ile Phe Ser Ser Gln Pro Gly His Thr Pro 45 50 55	317
25	CAT CCA GCC GCA TCC CGC GAC CCG GTC GCC AGG ACC TCG CCG CTG CAG His Pro Ala Ala Ser Arg Asp Pro Val Ala Arg Thr Ser Pro Leu Gln 60 65 70	365
30	ACC CCG GCT GCC CCC GGC GCC GCC GCG GGG CCT GCG CTC AGC CCG GTG Thr Pro Ala Ala Pro Gly Ala Ala Ala Gly Pro Ala Leu Ser Pro Val 75 80 85	413
35	CCA CCT GTG GTC CAC CTG GCC CTC CGC CAA GCC GGC GAC GAC TTC TCC Pro Pro Val Val His Leu Ala Leu Arg Gln Ala Gly Asp Asp Phe Ser 90 95 100 105	461
40	CGC CGC TAC CGC GGC GAC TTC GCC GAG ATG TCC AGC CAG CTG CAC CTG Arg Arg Tyr Arg Gly Asp Phe Ala Glu Met Ser Ser Gln Leu His Leu 110 115 120	509
45	ACG CCC TTC ACC GCG CGG GGA CGC TTT GCC ACG GTG GTG GAG GAG CTC Thr Pro Phe Thr Ala Arg Gly Arg Phe Ala Thr Val Val Glu Glu Leu 125 130 135	557
50	TTC AGG GAC GGG GTG AAC TGG GGG AGG ATT GTG GCC TTC TTT GAG TTC Phe Arg Asp Gly Val Asn Trp Gly Arg Ile Val Ala Phe Phe Glu Phe 140 145 150	605
	GGT GGG GTC ATG TGT GTG GAG AGC GTC AAC CGG GAG ATG TCG CCC CTG Gly Gly Val Met Cys Val Glu Ser Val Asn Arg Glu Met Ser Pro Leu 155 160 165	653
	GTG GAC AAC ATC GCC CTG TGG ATG ACT GAG TAC CTG AAC CGG CAC CTG Val Asp Asn Ile Ala Leu Trp Met Thr Glu Tyr Leu Asn Arg His Leu 170 175 180 185	701



CAC ACC TGG ATC CAG GAT AAC GGA GGC TGG GTA GGT GCA TCT GGT GAT 749  
His Thr Trp Ile Gln Asp Asn Gly Gly Trp Val Gly Ala Ser Gly Asp  
190 195 200

5 GTG AGT CTG GGC TGAGGCCACA GGTCCGAGAT CGGGGGTTGG AGTGCGGGTG 801  
Val Ser Leu Gly  
205

10 GGCTCCTGGG CAATGGGAGG CTGTGGAGCC GGCGAAATAA AATCAGAGTT GTTGCTTCCC 861

GGCGTGTCCTACCTCCTCC TCTGGACAAA GCGTTCACTC CCAACCTGAC 911

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 205 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Met Ala His Ala Gly Arg Thr Gly Tyr Asp Asn Arg Glu Ile Val Met  
1 5 10 15

Lys Tyr Ile His Tyr Lys Leu Ser Gln Arg Gly Tyr Glu Trp Asp Ala  
20 25 30

Gly Asp Val Gly Ala Ala Pro Pro Gly Ala Ala Pro Ala Pro Gly Ile  
35 40 45

Phe Ser Ser Gln Pro Gly His Thr Pro His Pro Ala Ala Ser Arg Asp  
50 55 60

Pro Val Ala Arg Thr Ser Pro Leu Gln Thr Pro Ala Ala Pro Gly Ala  
65 70 75 80

Ala Ala Gly Pro Ala Leu Ser Pro Val Pro Pro Val Val His Leu Ala  
85 90 95

Leu Arg Gln Ala Gly Asp Asp Phe Ser Arg Arg Tyr Arg Gly Asp Phe  
100 105 110

Ala Glu Met Ser Ser Gln Leu His Leu Thr Pro Phe Thr Ala Arg Gly  
115 120 125

Arg Phe Ala Thr Val Val Glu Leu Phe Arg Asp Gly Val Asn Trp  
130 135 140

Gly Arg Ile Val Ala Phe Phe Glu Phe Gly Gly Val Met Cys Val Glu  
145 150 155 160

Ser Val Asn Arg Glu Met Ser Pro Leu Val Asp Asn Ile Ala Leu Trp  
165 170 175

5 Met Thr Glu Tyr Leu Asn Arg His Leu His Thr Trp Ile Gln Asp Asn  
180 185 190

Gly Gly Trp Val Gly Ala Ser Gly Asp Val Ser Leu Gly  
195 200 205

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